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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2008; month=2; day=5; hr=14; min=17; sec=45; ms=80;]

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Reviewer Comments:

<210> 7

<211> 54

<212> DNA

<213> Oligonucleotide Primer CF59

<400> 7

cgatagatct ttggataaga gagggccacc acctggcccc cctcgagttt cccc 54

The above <213> response is invalid, also similar responses were found in sequence id#'s 10 and 11. FYI, these responses can be inserted into section <220> to <223>.

Application No: 10584438 Version No: 1.0

Input Set:

Output Set:

Started: 2008-01-29 15:17:14.169
Finished: 2008-01-29 15:17:15.923
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 754 ms
Total Warnings: 20
Total Errors: 1
No. of SeqIDs Defined: 20
Actual SeqID Count: 20

Error code	Error Description
E 287	Invalid WIPO ST.2 date format; Use (YYYY-MM-DD) in <141>
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)

Input Set:

Output Set:

Started: 2008-01-29 15:17:14.169
Finished: 2008-01-29 15:17:15.923
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 754 ms
Total Warnings: 20
Total Errors: 1
No. of SeqIDs Defined: 20
Actual SeqID Count: 20

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

<210> 1
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Linker VC053

<400> 1
gatctttgga taagagagac gctcacaagt ccgaagtgc tcaccggt 48

<210> 2
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Linker VC054

<400> 2
ccttgaacct gtgaggcgact tcggacttgt gagcgtctct cttatccaaa 50

<210> 3
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Linker VC055

<400> 3
gatctttgga taagagagac gctcacaagt ccgaagtgc tcatcgat 48

<210> 4
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Linker VC056

<400> 4
ccttgaatcg atgaggcgact tcggacttgt gagcgtctct cttatccaaa 50

<210> 5
<211> 86
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Linker VC057

<400> 5
tcaaggaccc aggtgaggaa aacttcaagg cttgggtctt gatcgcttc gctcaatact 60
tgcaacaatg tccattcgaa gatcac 86

<210> 6

<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Linker VC058

<400> 6
gtgatcttcg aatggacatt gttgcaagta ttgagcgaaa gcgatcaaga ccaaaggcctt 60
gaagtttcc tcaccttaggt 80

<210> 7
<211> 54
<212> DNA
<213> Oligonucleotide Primer CF59

<400> 7
cgatagatct ttggataaga gagggccacc acctggcccc cctcgagttt cccc 54

<210> 8
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide linker SEQ ID 8

<400> 8
Gly Gly Gly Gly Ser
1 5

<210> 9
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide linker SEQ ID 9

<400> 9
Gly Gly Gly Ser
1

<210> 10
<211> 17
<212> PRT
<213> Stanniocalcin signal peptide sequence

<400> 10
Met Leu Gln Asn Ser Ala Val Leu Leu Leu Val Ile Ser Ala Ser
1 5 10 15

Ala

<210> 11
<211> 22

<212> PRT
<213> Consensus signal sequence

<400> 11
Met Pro Thr Trp Ala Trp Trp Leu Phe Leu Val Leu Leu Leu Ala Leu
1 5 10 15

Trp Ala Pro Ala Arg Gly
20

<210> 12
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Primer CF60

<400> 12
ggccatcgat gagcgacttc ggacttgtga gcgtccagcc gagtcttcag cagcagcagt 60
ccccctc 66

<210> 13
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Primer CF61

<400> 13
ccggccttag gcttacctgg gccaccacct ggcccccctc gagtttcccc 50

<210> 14
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Primer CF62

<400> 14
ggccaagctt attacagccg agtcttcagc agcagcagtc ccctc 45

<210> 15
<211> 2358
<212> DNA
<213> Artificial Sequence

<220>
<223> N-terminal IL11-albumin fusion

<400> 15
atgaagtggg ttttcatcggt ctccattttg ttcttggttct cctctgctta ctcttagatct 60
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caagctgttttgc tgggttttgc 2358

<210> 16
<211> 786
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal IIII-albumin fusion

```

<400>    16
Met Lys Trp Val Phe Ile Val Ser Ile Leu Phe Leu Phe Ser Ser Ala
      1          5          10          15

```

Tyr Ser Arg Ser Leu Asp Lys Arg Gly Pro Pro Pro Gly Pro Pro Arg
 20 25 30

Val Ser Pro Asp Pro Arg Ala Glu Leu Asp Ser Thr Val Leu Leu Thr
 35 40 45

Arg Ser Leu Leu Ala Asp Thr Arg Gln Leu Ala Ala Gln Leu Arg Asp
50 55 60

Lys Phe Pro Ala Asp Gly Asp His Asn Leu Asp Ser Leu Pro Thr Leu
65 70 75 80

Ala Met Ser Ala Gly Ala Leu Gly Ala Leu Gln Leu Pro Gly Val Leu
85 90 95

Thr Arg Leu Arg Ala Asp Leu Leu Ser Tyr Leu Arg His Val Gln Trp
100 105 110

Leu Arg Arg Ala Gly Gly Ser Ser Leu Lys Thr Leu Glu Pro Glu Leu
115 120 125

Gly Thr Leu Gln Ala Arg Leu Asp Arg Leu Leu Arg Arg Leu Gln Leu
130 135 140

Leu Met Ser Arg Leu Ala Leu Pro Gln Pro Pro Pro Asp Pro Pro Ala
145 150 155 160

Pro Pro Leu Ala Pro Pro Ser Ser Ala Trp Gly Gly Ile Arg Ala Ala
165 170 175

His Ala Ile Leu Gly Gly Leu His Leu Thr Leu Asp Trp Ala Val Arg
180 185 190

Gly Leu Leu Leu Leu Lys Thr Arg Leu Asp Ala His Lys Ser Glu Val
195 200 205

Ala His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val
210 215 220

Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His
225 230 235 240

Val Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala
245 250 255

Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly
260 265 270

Asp Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met
275 280 285

Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu
290 295 300

Gln His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu
305 310 315 320

Val Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu
325 330 335

Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala
340 345 350

Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu
355 360 365

Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp
370 375 380

Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys
385 390 395 400

Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala
405 410 415

Val Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val
420 425 430

Ser Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His
435 440 445

Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr
450 455 460

Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys
465 470 475 480

Glu Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn
485 490 495

Asp Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu
500 505 510

Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu
515 520 525

Gly Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val
530 535 540

Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys
545 550 555 560

Cys Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp
565 570 575

Glu Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn
580 585 590

Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu
595 600 605

Leu Val Arg Tyr Thr Lys Val Pro Gln Val Ser Thr Pro Thr Leu
610 615 620

Val Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys
625 630 635 640

His Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val
645 650 655

Val Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp
660 665 670

Arg Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys
675 680 685

Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn
690 695 700

Ala Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys
705 710 715 720

Glu Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His
725 730 735

Lys Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe
740 745 750

Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys
755 760 765

Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu
770 775 780

Gly Leu
785

<210> 17
<211> 762
<212> PRT
<213> Artificial Sequence

<220>
<223> Mature N-terminal IL11-albumin fusion

<400> 17
Gly Pro Pro Pro Gly Pro Pro Arg Val Ser Pro Asp Pro Arg Ala Glu
1 5 10 15

Leu Asp Ser Thr Val Leu Leu Thr Arg Ser Leu Leu Ala Asp Thr Arg
20 25 30

Gln Leu Ala Ala Gln Leu Arg Asp Lys Phe Pro Ala Asp Gly Asp His
35 40 45

Asn Leu Asp Ser Leu Pro Thr Leu Ala Met Ser Ala Gly Ala Leu Gly
50 55 60

Ala Leu Gln Leu Pro Gly Val Leu Thr Arg Leu Arg Ala Asp Leu Leu
65 70 75 80

Ser Tyr Leu Arg His Val Gln Trp Leu Arg Arg Ala Gly Gly Ser Ser
85 90 95

Leu Lys Thr Leu Glu Pro Glu Leu Gly Thr Leu Gln Ala Arg Leu Asp
100 105 110

Arg Leu Leu Arg Arg Leu Gln Leu Leu Met Ser Arg Leu Ala Leu Pro
115 120 125

Gln Pro Pro Pro Asp Pro Pro Ala Pro Pro Leu Ala Pro Pro Ser Ser
130 135 140

Ala Trp Gly Gly Ile Arg Ala Ala His Ala Ile Leu Gly Gly Leu His
145 150 155 160

Leu Thr Leu Asp Trp Ala Val Arg Gly Leu Leu Leu Lys Thr Arg
165 170 175

Leu Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly
180 185 190

Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu
195 200 205

Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr
210 215 220

Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp
225 230 235 240

Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr
245 250 255

Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu
260 265 270

Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn
275 280 285

Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe
290 295 300

His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala
305 310 315 320

Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys
325 330 335

Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala
340 345 350

Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala
355 360 365

Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly
370 375 380

Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe
385 390 395 400

Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr
405 410 415

Lys Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp
420 425 430

Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile
435 440 445

Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser
450 455 460

His Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro
465 470 475 480

Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr
485 490 495

Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala
500 505 510

Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys
515 520 525

Thr Tyr Glu Thr Thr Leu Glu Lys Cys